## SEQUENCE LISTING

<110> Sumitomo Chemical Co., Ltd.

<120> ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY TO CYTOKININ RECEPTOR

<130> P152622

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 3531

<212> DNA

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Pne		Pro	Ala	Pro	He		Asp	Glu	Tyr	Ala		Val	He	Phe	Ala	
	370					375					380					
000	<i>α</i>	a a t	~+ +	t 0.0	0 0 t	a <del>t</del>	or to	+ a a	~+ a	~~~			11			1000
Caa	gaa	acı	gıı	100	Cai	all	gıa	ıcg	gic	gac	aig	aıg	ıcı	gga	gaa	1200
Gln	Glu	Thr	Val	Sar	Hic	Πρ	Val	Sar	Val	Asp	Mot	Mot	Sor	C1w	C1n	
385	Ulu	1111	<b>va</b> 1	561	390	116	Val	361	vai	395	Mei	Met	261	біу		
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Бии	Suc	USI	Suu	uuc	arc	ııa	V 5 5	gua	uss	Sca	ica	55a	aaa	gga	618	1240
Glu	Asp	Arg	Glu	Asn	Ile	Leu	Arg	Ala	Arg	Ala	Ser	Glv	Lvs	Glv	Val	
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tta	aca	tct	cca	<u> </u>	ลูลช	ctt	ctt	ลลฮ	tca	aat	cat	c t t	ggt	grt t	gtg	1296
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Lys Val Leu Tyr Arg His Gln Asn Val Thr Arg Ser Glu Ile His Asp

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His Lys Glu Ser Ser Pro Gly Met Trp Thr Asn Tyr Gly Ile Thr Cys
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Ser Leu Ser Val Arg Ser Asp Lys Gln Glu Thr Arg Gly Leu Pro Trp
115 120 125

Asn	Leu	Gly	Leu	Gly	His	Ser	He	Ser	Ser	Thr	Ser	Cys	Me t	Cys	Gly
	130					135					140				
Asn	Leu	Glu	Pro	He	Leu	Gln	Gln	Pro	Glu	Asn	Leu	Glu	Glu	Glu	Asn
145					150					155					160
His	Glu	Glu	Gly	Leu	Glu	Gln	Gly	Leu	Ser	Ser	Tyr	Leu	Arg	Asn	Ala
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Trp	Trp	Cys	Leu	Ile	Leu	Gly	Val	Leu	Val	Cys	His	Lys	Ile	Tyr	Val
			180					185					190		
Ser	His	Ser	Lys	Ala	Arg	Gly	Glu	Arg	Lys	Glu	Lys	Val	His	Leu	Gln
		195					200					205			
Glu	Ala	Leu	Ala	Pro	Lys	Lys	Gln	Gln	Gln	Arg	Ala	Gln	Thr	Ser	Ser
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225					230					235					240
Gly	Gly	Val	Ser	Phe	Ser	Val	Trp	Trp	Phe	Trp	Asp	Thr	Asn	Glu	Glu
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Ile	lle	Met	Lys	Arg	Arg	Glu	Thr	Leu	Ala	Asn	Met	Cys	Asp	Glu	Arg
			260					265					270		
Ala	Arg	Val	Leu	Gln	Asp	Gln	Phe	Asn	Val	Ser	Leu	Asn	His	Val	His
		275					280					285			
Ala	Leu	Ser	He	Leu	Val	Ser	Thr	Phe	His	His	Gly	Lys	He	Pro	Ser
	290					295					300				
Ala	He	Asp	Gln	Arg	Thr	Phe	Glu	Glu	Tyr	Thr	Glu	Arg	Thr	Asn	Phe
305					310					315					320
Glu	Arg	Pro	Leu	Thr	Ser	Gly	Val	Ala	Tyr	Ala	Leu	Lys	Val	Pro	His
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Ser	Glu	Arg	Glu	Lys	Phe	Glu	Lys	Glu	His	Gly	Trp	Ala	Ile	Lys	Lys
			340					345					350		
Met	Glu	Thr	Glu	Asp	Gln	Thr	Val	Val	Gln	Asp	Cys	Val	Pro	Glu	Asn
		355					360					365			
Phe	Asp	Pro	Ala	Pro	Ile	Gln	Asp	Glu	Tyr	Ala	Pro	Val	He	Phe	Ala
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385					390					395					400
Glu	Asp	Arg	Glu	Asn	Ile	Leu	Arg	Ala	Arg	Ala	Ser	Gly	Lys	Gly	Val
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			420					425					430		
Leu	Thr	Phe	Ala	Val	Tyr	Asp	Thr	Ser	Leu	Pro	Pro	Asp	Ala	Thr	Glu
		435					440					445			
Glu	Gln	Arg	Val	Glu	Ala	Thr	Ile	Gly	Tyr	Leu	Gly	Ala	Ser	Tyr	Asp
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465					470					475					480
Thr	Ile	Ala	Val	Asp	Val	Tyr	Asp	Thr	Thr	Asn	Thr	Ser	Gly	Leu	Ile
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Lys	Met	Tyr	Gly	Ser	Glu	He	Gly	Asp	He	Ser	Glu	Gln	His	He	Ser
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705					710					715					720
Glu	Arg	Gly	His	Ile	Phe	He	Ser	Val	His	Leu	Ala	Asp	Glu	Val	Lys
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Asp	Leu	Ala	He	Gln	Glu	Phe	Thr	Gly	Leu	Arg	Ala	Leu	Val	He	Asp
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		]	1060					1065				]	1070		
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Met				Pro	His				Ala	Cys				Leu	Gln
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Me t	Pro 1090 Arg	Lys 1075 Glu	Pro Met	Asp Asn	Gly	Phe 1095	Phe 1080 Glu	Asp Ala	Thr Ser	Arg	Arg 1100	Met 1085 Val	Asp Arg	Glu Ala	Leu
Met Glu 1105	Pro 1090 Arg	Lys 1075 Glu Glu	Pro Met	Asp Asn	Gly Lys 1110	Phe 1095	Phe 1080 Glu Ile	Asp Ala Ala	Thr	Arg Gly	Arg 1100 Glu	Met 1085 Val Val	Asp Arg Ser	Glu	Leu Glu 1120
Met Glu 1105	Pro 1090 Arg	Lys 1075 Glu Glu	Pro Met Ile	Asp Asn	Gly Lys 1110	Phe 1095 Lys	Phe 1080 Glu Ile	Asp Ala His	Thr	Arg Gly	Arg 1100 Glu	Met 1085 Val Val	Asp Arg Ser	Glu	Leu Glu 1120
Met Glu 1105 Met	Pro 1090 Arg Dhe	Lys 1075 Glu Glu Cys	Pro Met Lys	Asp Asn Phe	Gly Lys 1110 Ser	Phe 1095 Lys	Phe 1080 Glu Ile	Asp Ala Ala	Thr Ser Val	Arg Gly 1115 Pro	Arg 1100 Glu Ile	Met 1085 Val Val	Asp Arg Ser	Glu Ala Met	Leu Glu 1120 Thr
Met Glu 1105 Met	Pro 1090 Arg Dhe	Lys 1075 Glu Glu Val	Pro Met Lys	Asp Asn Phe	Gly Lys 1110 Ser	Phe 1095 Lys Ser	Phe 1080 Glu Ile Trp	Asp Ala Ala	Thr Ser Val	Arg Gly 1115 Pro	Arg 1100 Glu Ile	Met 1085 Val Val Leu	Asp Arg Ser	Glu Ala Met	Leu Glu 1120 Thr
Met Glu 1105 Met	Pro 1090 Arg The	Lys 1075 Glu Glu Cys	Pro Met Lys Ile	Asp Asn Phe 1125 Gln	Gly Lys 1110 Ser	Phe 1095 Lys Ser	Phe 1080 Glu Ile Trp	Asp Ala Ala His Glu	Thr Ser Val 1130 Glu	Arg Gly 1115 Pro	Arg 1100 Glu Ile Met	Met 1085 Val Val Leu	Asp Arg Ser Ala Cys	Glu Ala Met 1135 Gly	Leu Glu 1120 Thr

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Phe Trp Met Leu Cys Cys Trp Phe Val Ser Trp Phe Val Asp Asn Gly
20 25 30

atc gag gac aag tot ggt ott tta gtt ggc tot gtc ggt gat ott gag 144

	al Gly Asp Leu Glu	Ser Val	Gly	Val	Leu	Leu	Gly	Ser	Lys	Asp	Glu	He
	45				40					35		
192	ao ato too tir too	220 22	ລລຕ	ກາຕ	າລຕ	tta	200	a a t	n t a	a a cr	n a t	0.00
102	ag atg tgg ttc tgg	aac aa	aag	aag	aag	ııg	acg	acı	aig	aag	acı	aag
	ys Met Trp Phe Trp	Asn Lys	Lys	Lys	Lys	Leu	Thr	Thr	Met	Lys	Thr	Lys
	60	60				55					50	
240	igt ttc tct tat cag	ccg ag	atc	ลลซ	ctc	gga	გთი	age	tet	ate	220	aat
		008 48	uro	uug		55u	ugo	ago	101	aic	aag	aaı
		_										
	er Phe Ser Tyr Gln	Pro Sei	He	Lys	Leu	Gly	Ser	Ser	Ser	Ile	Lys	Asn
	80	75					70					65
288	tgg agg aag ctt gtg	tgg tg	gcg	aag	aac	ttc	aaa	gtt	tet	ggc	ctt	ttt
		-00	0.0	0	<b>u</b> v		444	0		66°		
	A T Tau Wal	m m	. 1	<del>.</del>		<b>7.</b> 1	_		_		_	
	rp Arg Lys Leu Val	Trp Trp	Ala	Lys	Asn	Phe	Lys	Val	Ser	Gly	Leu	Phe
	95		90					85				
336	att tgg acg ttt tgg	tct at	gtc	ttg	gtc	t gg	ttc	gtc	gtt	tgg	gtt	gtg
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	le Trp Thr Phe Trp	Ser 110	vai	Leu	Val	Trp	Phe	Val	Val	Trp	Val	Val
	110			105					100			
384	gag acg cta gct agt	aaa ga	gagg	g aag	gag	atg	gct	caa	tcg	agc	ttt	tac

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Tyr	Phe	Ser	Ser	Gln	Ala	Met	Glu	Lys	Arg	Lys	Glu	Thr	Leu	Ala S	Ser	
		115					120					125				
atg	tgt	gat	gag	aga	gct	cgt	atg	ctg	cag	gat	cag	ttc	aac	gtt	agc	432
Met	Cys	Asp	Glu	Arg	Ala	Arg	Met	Leu	Gln	Asp	Gln	Phe	Asn	Val :	Ser	
	130					135					140					
atg	aat	cat	gtt	caa	gcc	atg	tct	atc	ttg	atc	tca	acc	ttc	cac	cat	480
Met	Asn	His	Val	Gln	Ala	Met	Ser	He	Leu	Ile	Ser	Thr	Phe	His	His	
145					150					155					160	
110																
<b>~</b> ~	0.00	n t t	oot	tot	ac t	ato	gat	cag	r 202	a c a	tto	· tca	gag	tac	ac t	528
ggc	aag	ali	CCI	ıcı	gcı	aic	gai	. ταε	, ugu	. 400		, , , ,	, 6 <sub>4</sub> 6	, tuo		<b>.</b>
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Gly	Lys	He	Pro			116	Asp	GIII			rne	261	GIU	Tyr	1111	
				165					170					175		
gat	aga	ac t	tcc	ttt	gag	gage	g cct	tcti	t act	ago	ggg	g gta	gct	tat	gct	576
Asp	Arg	Thr	Ser	Phe	Glu	Arg	Pro	Leu	Thr	Ser	Gly	Val	Ala	Tyr	Ala	
			180					185					190			
ato	, yaa	gtø	e cto	cat	t toa	ı gas	g ags	g gaa	a gag	g tte	c ga	g agg	g caa	ı caa	ggt	624
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Met Arg Val Leu His Ser Glu Arg Glu Glu Phe Glu Arg Gln Gln Gly

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tgg	act	att	agg	aag	atg	tat	tct	ctt	gaa	caa	aac	cca	a gti	t cac	aag	672
Trp	Thr 210		Arg	Lys	Met	Tyr 215	Ser	Leu	Glu	Gln	Asn 220	Pro	Val	His	Lys	
gat	gac	tat	gac	ctg	gaa	gct	ttg	gaa	cca	tcc	cct	gto	c caa	ı gaa	gag	720
Asp 225	Asp	Tyr	Asp	Leu	Glu 230	Ala	Leu	Glu	Pro	Ser 235	Pro	Val	Gln	Glu	Glu 240	
tac	gct	cca	gtc	atc	ttt	gct	cag	gac	act	gtt	tct	cac	gtt	gtt	tct	768
Tyr	Ala	Pro	Val	Ile 245	Phe	Ala	Gln	Asp	Thr 250	Val	Ser	His	Val	Val 255	Ser	
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Leu	Asp	Met	Leu 260	Ser	Gly	Lys	Glu	Asp 265	Arg	Glu	Asn	Val	Leu 270	Arg	Ala	
agg	agt	tca	ggt	aaa	ggg	gtt	ttg	aca	gc t	cct	ttc	cca	ttg	ata	aag	864
Arg	Ser	Ser	Glv	Lvs	Glv	Val	Len	Th <i>r</i>	Ala	Pro	Phe	Pro	ľρn	Ile	Ive	

aca	aat	aga	ctt	ggg	gtg	atc	ctg	aca	ttt	gca	gtg	g tac	aa;	g ag	a ga	.t	912
Thr	Asn 290	Arg	Leu	Gly	Val	Ile 295	Leu	Thr	Phe	Ala	Val 300	Tyr	Lys	Arg	g Asp	)	
ctc	ccc	tcc	aat	gca	acg	cca	aaa	gag	aga	att	gag	g gc t	ac	t aa	c gg	g	960
Leu 305	Pro	Ser	Asn	Ala	Thr 310	Pro	Lys	Glu	Arg	Ile 315	Glu	Ala	Thr	Asn	Gly 320		
tat	ctc	ggg	gga	gtg	ttt	gac	att	gag	tcc	ctg	gta	. gaa	. aac	e tt	g ct	t	1008
Tyr	Leu	Gly	Gly	Val 325	Phe	Asp	Ile	Glu	Ser 330	Leu	Val	Glu	Asn	Leu 335			
caa	cag	ctg	gct	agc	aag	caa	acg	a t t	ctt	gtc	aat	gtg	tac	ga	t at	c	1056
Gln	Gln	Leu	Ala 340	Ser	Lys	Gln		Ile 345	Leu	Val	Asn	Val	Tyr 350	Asp	Ile		-
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Thr	Asn	His 355	Ser	Gln	Pro		Ser 360	Met	Tyr	Gly		Asn 365	Val	Ser	Ala		

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Lys 385	His	Glu	Met	Arg	Cys 390	Arg	Phe	Lys	Gln	Lys 395	Pro	Pro	Trp	Pro	Val 400		
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Leu	Ser	Met	Val	Thr 405	Ser	Phe	Gly	Ile	Leu 410	Val	Ile	Ala	Leu	Leu 415	Val		
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Ala	His	Ile	Ile 420	His	Ala	Thr	Val	Ser 425	Arg	Ile	His		Val 430	Glu	Glu		
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Asp		Asp 435	Lys	Met	Lys		Leu 440	Lys	Lys	Lys		Glu 445	Ala	Ala	Asp		
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Leu	Asp	Val	Thr	Gln	Gln	Asp	Tyr	Val	Arg	Thr	Ala	Gln	Ala	Ser	Gly	
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	Ger		0.1													
Lvs	Ala	Len	Val	Ser	Leu	He	Asn	Glu	Val	Leu	Asp	Gln	Ala	Lys	He	
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C1	Com	C1	Ι ***	Lou	Cla	Lou	Clu	Clu	Val	Ara	Dhο	Asn	Leu	Δrσ	Glv	
GIU	ser			Leu	GIU	Leu			Val	ΛIĞ	THE			шБ	dly	
		515					520					525	ı			
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Ile Leu	ı Asp	Asp	Val	Leu	Ser	Leu	Phe	Ser	Ser	Lys	Ser	Gln	Gln	Lys		
530	)				535					540						
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Gly Va	l Glu	Leu	Ala	Val	Tyr	Ile	Ser	Asp	Arg	Val	Pro	Asp	Met	Leu		
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lle Gl	y Asp	Pro	Gly	Arg	Phe	Arg	Gln	He	Leu	Thr	Asn	Leu	Met	Gly		
			565					570					575	•		
aat tc	c att	aag	ttc	ac t	gag	aaa	gga	cac	ato	ttt	gta	act	gt	t cat	t 177	6
Asn Se	r Ile	Lys	Phe	Thr	Glu	Lys	Gly	His	He	Phe	Val	Thr	Val	His		
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Leu Va	l Asp	Glu	Leu	Phe	Glu	Ser	Ile	Asp	Gly	Glu	Thr	Ala	Sei	s Ser		
	595	<b>,</b>				600					605					
ccg ga	a ag	t aca	cte	g agt	ggg	ct t	cca	gti	t gca	a ga	c cg	g ca	g ag	g ag	c 187	4

Pro Glu Ser Thr Leu Ser Gly Leu Pro Val Ala Asp Arg Gln Arg Ser

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tgg	gaa	aac	ttt	aaa	gct	ttc	agc	tcc	aac	ggg	g cai	t cgg	g ag	c tt	tt g	aa	192
Trp 625		Asn	Phe	Lys	Ala 630	Phe	Ser	Ser	Asn	Gly 635	His	Arg	Ser	Phe			
020					000					000					64	ŧU	
cca	tct	ccc	cct	gat	ata	aac	cta	atc	gtc	tca	gtt	gag	ga1	t ac	et g	gc	1968
Pro	Ser	Pro	Pro	Asp 645	Ile	Asn	Leu	Ile		Ser	Val	Glu	Asp		_	У	
				040					650					655	)		
gta	ggg	atc	cct	gta	gaa	gcg	cag	tcc	cgt	att	ttt	acg	cct	tt	c a	tg	2016
Val	Gly	Ile		Val	Glu	Ala			Arg	Ile	Phe	Thr		Phe	e Me	t	
			660					665					670				
caa	gtc	gga	cca	tcc	ata	tcc	agg	acg	cat	gga	ggc	aca	gga	at	t gg	ga	2064
Gln	Val		Pro	Ser	He			Thr	His	Gly			Gly	Ile	Gl	у	
		675					680					685					

ctt agc ata agc aaa tgt cta gtt gga ctg atg aag gga gaa att gga Leu Ser Ile Ser Lys Cys Leu Val Gly Leu Met Lys Gly Glu Ile Gly 

ttc	tcg	agt	act	ccc	aag	gtt	ggg	tcc	aca	ttc	aca	ttt	ac t	gc	t gta	,	2160
Phe	Ser	Ser	Thr	Pro	Lys	Val	Gly	Ser	Thr	Phe	Thr	Phe	Thr	Ala	Val	•	
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ttt	tcc	aat	ggg	atg	caa	cca	gct	gaa	aga	aag	aat	gac	<b>aa</b> 0	aa	c cag	•	2208
Phe	Ser	Asn	Gly	Met 725	Gln	Pro	Ala	Glu	Arg 730	Lys	Asn	Asp	Asn	Asn 735	Gln		
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Pro	Ile	Phe	Ser 740	Glu	Phe	Arg	Gly	Met 745	Lys	Ala	Val	Val	Val 750	Asp	His		
agg	cct	gca	agg	gca	aaa	gtc	tcg	tgg	tac	cat	t t t	cag	g cgt	t ct	t gga	l	2304
Arg	Pro	Ala 755	Arg	Ala	Lys	Val	Ser 760	Trp	Tyr	His	Phe	Gln 765	Arg	Leu	Gly		
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Ile	Arg 770		Glu	Val	Val	Pro 775	Arg	Val	Glu	Gln	Ala 780		His	Tyr	Leu		

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Lys 785	Ile	Gly	Thr	Thr	Thr 790	Val	Asn	Met	Ile	Leu 795	Ile	Glu	Gln	Glu	Ile 800	
tgg	aat	agg	gaa	gca	gat	gat	ttc	att	aaa	aag	cta	cag	aaa	gac	cct	2448
Trp	Asn	Arg	Glu	Ala 805	Asp	Asp	Phe	Ile	Lys 810	Lys	Leu	Gln		Asp 815	Pro	
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Val	Lys 850		Leu	Arg	Ala	Ser 855	Met	Leu	Ala	Ala	Thr 860	Leu	Gln	Arg	Gly	

ttg ggt att gga atc aga gaa cca cct caa cac aag gga cct cct gct

Leu	Gly	He	Gly	116	Arg	GIU	Pro	Pro	G I II	HIS	Lys	GIY	rio	PIO	Ala	
865					870					875					880	
ttg	att	ctc	agg	aat	ctt	ctc	ctt	ggt	aga	aaa	att	tta	atc	gtg	gat	2688
Leu	Ile	Leu	Arg	As n 885	Leu	Leu	Leu	Gly	Arg 890	Lys	Ile	Leu	Ile	Val 895	Asp	
gat	aac.	aac	gta	aac	ctc	aga	gtg	gca	gcg	gga	gc t	ctg	aaa	. aag	g tac	2736
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Gly	Ala	Asp 915	Val	Val	Cys	Ala	Glu 920	Ser	Gly	Ile	Lys	Ala 925	Ile	Ser	Leu	
ctt	aag	cca	cct	cac	gag	ttt	gat	gct	tgc	ttc	atg	gac	ati	. cas	g atg	2832
Leu	Lys 930		Pro	His	Glu	Phe 935	Asp	Ala	Cys	Phe	Me t 940	Asp	Ile	Gln	Met	
cca	gaa	atg	gat	gga	ttt	gaa	get	aca	agg	aga	ata	. cga	ı gai	t ats	g gaa	2880

Pro	Glu	Met	Asp	Gly	Phe	Glu	Ala	Thr	Arg	Arg	lle.	Arg A	Asp N	net (	J I U	
945					950					955				(	960	
gag	gag	atg	aac	aag	aga	ata	aag	aat	ggg	gag	gct	ttg	ata	gta	gag	2928
Glu	Glu	Met	Asn	Lys 965	Arg	Ile	Lys		Gly 970	Glu	Ala	Leu		Val ( 975	Glu	
aac	ggt	aac	aaa	aca	agc	t gg	cat	ctt	ccg	gta	tta	gca	atg	acg	gca	2976
Asn	Gly	Asn	Lys 980		Ser	Trp	His	Leu 985	Pro	Val	Leu	Ala	Me t 990	Thr	Ala	
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Asp	Val	Ile 995		Ala	Thr		Glu 1000	Glu	Cys	Leu		Cys 1005	Gly	Met	Asp	
ggg	tat	gta	tca	ı aaa	ı cca	. ttt	gaa	gca	gag	cag	; ctg	g tac	agg	gaa	gtt	3072
	Tyr 1010		Ser	Lys		Phe 1015		Ala	Glu		Leu 1020	Tyr	Arg	Glu	Val	
tct	cgo	: tt1	tto	c aa	t tcg	g cct	tea	ı gat	aca	ı gaa	ı tca	a taa				3111
Ser	Arg	g Phe	Phe	e Asr	ı Ser	Pro	Ser	Asp	Thr	Glu	Ser					

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<213> Arabidopsis thaliana

<400> 4

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Phe Trp Met Leu Cys Cys Trp Phe Val Ser Trp Phe Val Asp Asn Gly 

Ile Glu Asp Lys Ser Gly Leu Leu Val Gly Ser Val Gly Asp Leu Glu 

Lys Thr Lys Met Thr Thr Leu Lys Lys Lys Asn Lys Met Trp Phe Trp 

Asn Lys Ile Ser Ser Ser Gly Leu Lys Ile Pro Ser Phe Ser Tyr Gln 

Phe Leu Gly Ser Val Lys Phe Asn Lys Ala Trp Trp Arg Lys Leu Val 

Val Val Trp Val Val Phe Trp Val Leu Val Ser Ile Trp Thr Phe Trp 

Tyr Phe Ser Ser Gln Ala Met Glu Lys Arg Lys Glu Thr Leu Ala Ser 

Met Cys Asp Glu Arg Ala Arg Met Leu Gln Asp Gln Phe Asn Val Ser

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Met	Asn	His	Val	Gln	Ala	Met	Ser	He	Leu	Ile	Ser	Thr	Phe	His	His
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Gly	Lys	Ile	Pro	Ser	Ala	Ile	Asp	Gln	Arg	Thr	Phe	Ser	Glu	Tyr	Thr
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Asp	Arg	Thr	Ser	Phe	Glu	Arg	Pro	Leu	Thr	Ser	Gly	Val	Ala	Tyr	Ala
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Tyr	Ala	Pro	Val	Ile	Phe	Ala	Gln	Asp	Thr	Val	Ser	His	Val	Val	Ser
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Thr	Asn	Arg	Leu	Gly	Val	.Ile	Leu	Thr	Phe	Ala	Val	Tyr	Lys	Arg	Asp
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Gln	Gln	Len	Ala	Ser	Lvs	Gln	Thr	He	Leu	Val	Asn	Val	Tvr	Asp	He

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Thr	Asn	His	Ser	Gln	Pro	He	Ser	Met	Tyr	Gly	Thr	Asn	Val	Ser	Ala
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Asp	Gly	Leu	Glu	Arg	Val	Ser	Pro	Leu	Ile	Phe	Gly	Asp	Pro	Leu	Arg
	370					375					380				
Lys	His	Glu	Met	Arg	Cys	Arg	Phe	Lys	Gln	Lys	Pro	Pro	Trp	Pro	Val
385					390					395					400
Leu	Ser	Me t	Val	Thr	Ser	Phe	Gly	Ile	Leu	Val	Ile	Ala	Leu	Leu	Val
				405					410					415	
Ala	His	Ile	Ile	His	Ala	Thr	Val	Ser	Arg	Ile	His	Lys	Val	Glu	Glu
			420					425					430		
Asp	Cys	Asp	Lys	Met	Lys	Gln	Leu	Lys	Lys	Lys	Ala	Glu	Ala	Ala	Asp
		435					440					445			
Val	Ala	Lys	Ser	Gln	Phe	Leu	Ala	Thr	Val	Ser	His	Glu	Ile	Arg	Thr
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Pro	Met	Asn	Gly	Val	Leu	Gly	Met	Leu	His	Met	Leu	Met	Asp	Thr	Glu
465					470					475					480
Leu	Asp	Val	Thr	Gln	Gln	Asp	Tyr	Val	Arg	Thr	Ala	Gln	Ala	Ser	Gly
				485					490					495	
Lys	Ala	Leu	Val	Ser	Leu	Ile	Asn	Glu	Val	Leu	Asp	Gln	Ala	Lys	Ile
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Glu	Ser	Gly	Lys	Leu	Glu	Leu	Glu	Glu	Val	Arg	Phe	Asp	Leu	Arg	Gly
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Ile	Leu	Asp	Asp	Val	Leu	Ser	Leu	Phe	Ser	Ser	Lys	Ser	Gln	Gln	Lys
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Glv	Val	Glu	Len	Ala	Val	Tvr	He	Ser	Asp	Arg	Val	Pro	Asp	Met	Leu

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Leu	Val	Asp	Glu	Leu	Phe	Glu	Ser	Ile	Asp	Gly	Glu	Thr	Ala	Ser	Ser
		595					600					605			
Pro	Glu	Ser	Thr	Leu	Ser	Gly	Leu	Pro	Val	Ala	Asp	Arg	Gln	Arg	Ser
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625					630					635					640
Pro	Ser	Pro	Pro	Asp	Ile	Asn	Leu	Ile	Val	Ser	Val	Glu	Asp	Thr	Gly
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Val	Gly	Ile	Pro	Val	Glu	Ala	Gln	Ser	Arg	Ile	Phe	Thr	Pro	Phe	Met
			660					665					670		
Gln	Val	Gly	Pro	Ser	Ile	Ser	Arg	Thr	His	Gly	Gly	Thr	Gly	Ile	Gly
		675					680					685			
Leu	Ser	Ile	Ser	Lys	Cys	Leu	Val	Gly	Leu	Met	Lys	Gly	Glu	Ile	Gly
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Phe	Ser	Ser	Thr	Pro	Lys	Val	Gly	Ser	Thr	Phe	Thr	Phe	Thr	Ala	Val
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Phe	Ser	Asn	Gly	Met	Gln	Pro	Ala	Glu	Arg	Lys	Asn	Asp	Asn	Asn	Gln
				725					730					735	
Pro	Ile	Phe	Ser	Glu	Phe	Arg	Gly	Me t	Lys	Ala	Val	Val	Val	Asp	His
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Arg	Pro	Ala	Arg	Ala	Lys	Val	Ser	Trp	Tyr	His	Phe	Gln	Arg	Leu	Gly

		755					760					765			
Ile	Arg	Val	Glu	Val	Val	Pro	Arg	Val	Glu	Gln	Ala	Leu	His	Tyr	Leu
	770					775					780				
Lys	Ile	Gly	Thr	Thr	Thr	Val	Asn	Met	Ile	Leu	Ile	Glu	Gln	Glu	Ile
785					790					795					800
Trp	Asn	Arg	Glu	Ala	Asp	Asp	Phe	Ile	Lys	Lys	Leu	Gln	Lys	Asp	Pro
				805					810					815	
Leu	Phe	Leu	Ser	Pro	Lys	Leu	Ile	Leu	Leu	Ala	Asn	Ser	Val	Glu	Ser
			820					825					830		
Ser	Ile	Ser	Glu	Ala	Leu	Cys	Thr	Gly	Ile	Asp	Pro	Pro	Ile	Val	Ile
		835					840					845			
Val	Lys	Pro	Leu	Arg	Ala	Ser	Met	Leu	Ala	Ala	Thr	Leu	Gln	Arg	Gly
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865					870					875					880
Leu	Ile	Leu	Arg	Asn	Leu	Leu	Leu	Gly	Arg	Lys	Ile	Leu	Ile	Val	Asp
				885					890					895	
Asp	Asn	Asn	Val	Asn	Leu	Arg	Val	Ala	Ala	Gly	Ala	Leu	Lys	Lys	Tyr
			900					905					910		
Gly	Ala	Asp	Val	Val	Cys	Ala	Glu	Ser	Gly	Ile	Lys	Ala	He	Ser	Leu
		915					920					925			
Leu	Lys	Pro	Pro	His	Glu	Phe	Asp	Ala	Cys	Phe	Met	Asp	Ile	Gln	Met
	930					935					940			**	
Pro	Glu	Met	Asp	Gly	Phe	Glu	Ala	Thr	Arg	Arg	lle	Arg	Asp	Met	Glu
945					950					955					960
Glu	Glu	Met	Asn	Lvs	Arg	He	Lvs	Asn	Glv	Glu	Ala	Leu	Ile	Val	Glu

965 970 975 Asn Gly Asn Lys Thr Ser Trp His Leu Pro Val Leu Ala Met Thr Ala 980 985990 Asp Val Ile Gln Ala Thr His Glu Glu Cys Leu Lys Cys Gly Met Asp 995 1000 1005 Gly Tyr Val Ser Lys Pro Phe Glu Ala Glu Gln Leu Tyr Arg Glu Val 1010 1015 1020 Ser Arg Phe Phe Asn Ser Pro Ser Asp Thr Glu Ser

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Arg	Ile	Glu	Ile 20	Ser	Asp	Ser	Glu	Ser 25	Leu	Glu	Asn	Leu	Lys 30	Ser	Ser	
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Asp	Phe	Tyr 35	Gln	Leu	Gly	Gly	Gly 40	Gly	Ala	Leu	Asn	Ser 45	Ser	Glu	Lys	
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ccg	aga	aag	atc	gat	ttt	t gg	cgt	tcg	ggg	ttg	atg	ggt	ttt	gcg	g aag	192
Pro	Arg 50	Lys	Ile	Asp	Phe	Trp 55	Arg	Ser	Gly	Leu	Met 60	Gly	Phe	Ala	Lys	
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Met	Gln	Gln	Gln	Gln	Gln 70	Leu	Gln	His	Ser	Val 75	Ala	Val	Lys	Met	Asn 80	
aat	aat	aat	aat	aac	gat	cta	atg	ggt	aat	aaa	aaa	ı ggg	g tca	ı acı	ttc	288
Asn	Asn	Asn	Asn	Asn 85		Leu	Met	Gly	Asn 90	Lys	Lys	Gly	Ser	Thr 95	Phe	

ata	caa	gaa	cat	cga	gca	ttg	tta	cca	aaa	gct	ttg	att	ctg	tgg	atc	336
Ile	Gln	Glu	His 100	Arg	Ala	Leu	Leu	Pro 105	Lys	Ala	Leu	Ile	Leu 110	Trp	Ile	
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Ala	Asn 130	Lys	Ile	Arg	Arg	Glu 135	Glu	Val	Leu	Val	Ser 140	Met	Cys	Asp (	Gln	
aga	gct	aga	atg	ttg	cag	gat	caa	t t t	agt	gtt	agt	gtt	aat	cat	gtt	480
Arg 145	Ala	Arg	Met	Leu	Gln 150	Asp	Gln	Phe	Ser	Val 155	Ser	Val	Asn	His Y	Val 160	
cat	gct	ttg	gct	att	ctc	gtc	tcc	ac t	ttt	cat	tac	cac	aag	aac	cct	528
His	Ala	Leu	Ala	Ile 165	Leu	Val	Ser	Thr	Phe 170	His	Tyr	His	Lys	Asn l 175	Pro	

Ser	Ala	He	Asp	Gln	Glu	Thr	Phe	Ala	Glu	Tyr	Thr	Ala	Arg	Thr A	Ala	
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Phe	Glu	Arg	Pro	Leu	Leu	Ser	Gly	Val	Ala	Tyr	Ala	Glu	Lys	Val '	Val	
		195					200					205				
aat	ttt	gag	agg	gag	atg	ttt	gag	cgg	cag	cac	aat	tgg	ggti	ata	aag	672
												<b>m</b>	<b>T</b> 7 1	<b>7</b> 1	<b>.</b>	
Asn		Glu	Arg	Glu	Met		Glu	Arg	GIn	HIS		Trp	Val	Ile	LYS	
	210					215					220					
						4	4	~	4 است			<b>~</b> 0.4	* to:	t mat	a a t	720
aca	atg	gat	aga	gga	gag	ccı	ıca	ccg	gii	agg	gaı	gas	z ia	t gc t	CCI	120
Thr	Mot	Acn	Ara	Cly	Glu	Pro	Ser	Pro	Val	Arø	Asn	Glu	Tvr	Ala	Pro	
225	Met	лэр	MIG	uly	230	110	JCI	110	, 41	235	Пор	Ola	1,1		240	
220					200					200						
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Gly	Lys	Ala	Val	Leu	Thr	Ser	Pro	Phe	Arg	Leu	Leu	Glu	Thr	His	His	
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Leu	Gly	Val	Val	Leu	Thr	Phe	Pro	Val	Tyr	Lys	Ser	Ser	Leu	Pro	Glu	
	290					295					300					

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Asn Pro	Thr Val	Glu Glu Arg	Ile Ala Ala	Thr Ala Gly Tyr l	Leu Gly
305		310		315	320

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Gly Ala Phe As	sp Val Glu Ser Leu Val	Glu Asn Leu Leu Gly	Gln Leu
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gct ggt aac caa gca ata gtt gtg cat gtg tat gat atc acc aat gca 1056 Ala Gly Asn Gln Ala Ile Val Val His Val Tyr Asp Ile Thr Asn Ala

240	2.4.5	250
340	345	350

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Ser	Asp	Pro 355	Leu	Val	Met	Tyr	Gly 360	Asn	Gln	Asp	Glu	Glu 365	Ala	Asp	Arg		
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Ser	Leu 370	Ser	His	Glu	Ser	Lys 375	Leu	Asp	Phe	Gly	Asp 380	Pro	Phe	Arg	Lys		
cat	aag	atg	ata	tgc	agg	tac	cac	caa	aag	gca	cca	ata	ı cca	att §	g aat	<b>t</b> :	1200
His 385	Lys	Met	Ile		Arg 390	Tyr	His	Gln	Lys	Ala 395	Pro	Ile	Pro	Leu	Asn 400		
gtg	ctc	aca	ac t	gtg	cca	ttg	ttc	ttt	gcg	att	ggt	ttc	ttg	g gtg	g ggt	: 1	248
Val	Leu	Thr		Val 405	Pro	Leu	Phe	Phe	Ala 410	Ile	Gly	Phe	Leu	Val 415	Gly		
tat	ata	ctg	tat	ggt	gca	gc t	atg	cac	ata	gta	aaa	gtc	gaa	gat	gat	1	296
ſyr	Ile		Tyr 420	Gly	Ala	Ala		His 425	Ile	Val	Lys	Val	Glu 430	Asp	Asp		

ttc	cat	gaa	atg	caa	gag	ctt	aaa	gtg	cga	gca	gaa	gct	gc t	ga	t gt	c	1344
Phe	His	Glu 435	Met	Gln	Glu	Leu	Lys 440	Val	Arg	Ala	Glu	Ala 445	Ala	Asp	Val		
gct	aaa	tcg	cag	ttt	ctt	gct	acc	gtg	tct	cac	gag	atc	agg	ac:	a cca	a	1392
Ala	Lys 450	Ser	Gln	Phe	Leu	Ala 455	Thr	Val	Ser	His	Glu 460	Ile	Arg	Thr	Pro		
atg	aat	ggc	att	ctc	gga	atg	ctt	gc t	atg	ctc	cta	gat	aca	gaa	a cta	a	1440
Met 465	Asn	Gly	Ile	Leu	Gly 470	Met	Leu	Ala	Met	Leu 475	Leu	Asp	Thr	Glu	Leu 480		
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Ser	Ser	Thr	Gln	Arg 485	Asp	Tyr	Ala	Gln	Thr 490	Ala	Gln	Val	Cys	Gly 495			
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Ala	Leu	Ile	Ala 500	Leu	Ile	Asn	Glu	Val	Leu	Asp	Arg	Ala	Lys 510	Ile	Glu		

gc t	gga	aag	ctg	gag	ttg	gaa	tca	gta	cca	ttt	gat	atc	cgt	tca	ata	1584
Ala	Gly	Lys 515	Leu	Glu	Leu	Glu	Ser 520	Val	Pro	Phe	Asp	Ile 525	Arg	Ser	Ile	
ttg	gat	gat	gtc	ctt	tct	cta	ttc	tct	gag	gag	tca	agg	aac	aaa	ı ggc	1632
Leu	Asp 530	Asp	Val	Leu	Ser	Leu 535	Phe	Ser	Glu	Glu	Ser 540	Arg	Asn	Lys	Gly	
att	gag	ctc	gcg	gtt	ttc	gtt	tca	gac	aaa	gta	cca	gag	ata	gto	c aaa	1680
Ile 545	Glu	Leu	Ala	Val	Phe 550	Val	Ser	Asp	Lys	Val 555	Pro	Glu	He	Val	Lys 560	
gga	gat	tca	ggg	aga	ttt	aga	cag	; ata	ato	ata:	aac	ctt	gtt	gg	a aat	1728
Gly	Asp	Ser	Gly	Arg 565		Arg	Gln	Ile	Ile 570		Asn	Leu	Val	Gly 575	Asn	
tcg	gtt	aaa	ıtto	aca	gag	aaa	ı gga	ı cai	t ato	; tti	gti	t aaa	gto	c ca	t ctt	1776
Ser	Val	Lys	Phe 580		Glu	Lys	Gly	His 585		Phe	Val	Lys	Val 590		Leu	

gcg gaa caa tca aaa gat gaa tct gaa ccg aaa aat gca ttg aat ggt 1824

Ala	Glu	Gln	Ser	Lys	Asp	Glu	Ser	Glu	Pro	Lys	Asn	Ala	Leu	Asn	Gly	
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gga	gtg	tct	gaa	gaa	atg	atc	gtt	gtt	tcc	aaa	cag	tca	agt	tac	aac	1872
Gly	Val	Ser	Glu	Glu	Met	He	Val	Val	Ser	Lys	Gln	Ser	Ser	Tyr	Asn	
	610					615					620					
																•
aca	ttg	agc	ggt	tac	gaa	gct	gc t	gat	ggt	cgg	aat	agc	t gg	g gat	tca	1920
		Ü														
Thr	Leu	Ser	Glv	Tvr	Glu	Ala	Ala	Asp	Gly	Arg	Asn	Ser	Trp	Asp	Ser	
625			0 - 3	- <b>3</b> -	630			-		635					640	
020																
t t c	aag	cat	t t o	otc	tct	ឲ្យខ	្ ៤៦៦	cag	r tea	ı tta	ı teş	g gag	: tt1	t gat	att	1968
	, aag	Cai	ııs	, gro	101	545	, 546	, , ,	, •••			, 0	,	J		
Dha	e Lys	Uic	Lou	Val	Sar	Clu	Glu	Gln	Ser	Len	Ser	Glu	Phe	Asp	He	
rne	t Lys	піз	Leu			Giu	Gru	OIII	650		501	oru	1110	655		
				645					000					000		
			4 4		4			· + o.c	n n t /			o በድር	r aa	t at1		2016
tc	i agc	aaı	gii	agg	cii	aıg	ggu	, ica	1 410	gad	ı ga	υ αυξ	8 88	ı aı	t gga	2010
_	_		** 1			<b>3</b> .5	<b>T</b> 7 1	0	71.	C1	<b>A</b> a <b>n</b>	ጥե +	Clar	Ha	Clv	
Sei	r Ser	Asn			Leu	Met	val			GIU	ASP	1111			GIY	
			660	1				665	•				670			
																222
a t	c cct	tta	ı gti	gca	a caa	gge	c cg	t gts	g tt	t ats	g cc	gtt	tat	g ca	a gca	2064

Ile	Pro	Leu	Val	Ala	Gln	Gly	Arg	Val	Phe	Met	Pro	Phe	Met	Gln	Ala	
		675					680					685				
gat	გდი	trø	act	tca	ลฐล	aac	tat	gga	ggt	ac t	ggt	att	ggt	ttg	gagt	2112
5 ա ւ	ugo	• • • •	u o t	V U U		240		504	55,					_	-	
•	<b>.</b>	0	<b>TL</b>	C	A	Aan	Ттт	C1 <sub>11</sub>	C 1 17	Thr	Cly	Tla	Clv	Ι Δ11	Ser	
Asp	ser	ser	1111	Ser	Arg		1 y 1	GIY	Gly	1111		116	GIY	LCu	561	
	690					695					700					
ata	agc	aag	tgt	ctt	gtt	gaa	ctt	atg	cgt	ggt	cag	g ata	ı aat	ttt	c ata	2160
Ile	Ser	Lys	Cys	Leu	Val	Glu	Leu	Met	Arg	Gly	Gln	He	Asn	Phe	Ile	
705		·	•		710					715					720	
100					110											
													<b>ل</b> یہ ا			9900
agc	cgg	cct	cat	att	gga	agc	acg	ttc	gg	, iic	ace	g gc	ıgı	ווו	a gag	2208
Ser	Arg	Pro	His	He	Gly	Ser	Thr	Phe	Trp	Phe	Thr	Ala	Val	Leu	Glu	
				725					730					735		
222	t or	gat	ลลล	tør	agt	ጀርያ	g att	: ลลด	c cat	ats	g aas	g aa	a cc	t aa	t gtg	2256
aaa	ıgu	<b>5</b> αι	uuu		ubi	5 Y E	,		. Ju		,	J				
			_	_	~		<b>.</b> .		***	<b>1</b>	Ţ	T	D	A	Wo 1	
Lys	Cys	Asp	Lys	Cys	Ser	Ala	He	Asn	HIS	met	Lys	Lys	PT0	ASN	Val	

gaa cac ttg cct tct act ttt aaa gga atg aaa gct ata gtt gtt gat 2304 Glu His Leu Pro Ser Thr Phe Lys Gly Met Lys Ala Ile Val Val Asp

745

740

75	55	760	765

gct aag cct gtt aga gct gct gtg act aga tac cat atg aaa aga ctc 2352

Ala Lys Pro Val Arg Ala Ala Val Thr Arg Tyr His Met Lys Arg Leu 770 775 780

gga atc aat gtt gat gtc gtg aca agt ctc aaa acc gct gtt gtt gca 2400

Gly Ile Asn Val Asp Val Val Thr Ser Leu Lys Thr Ala Val Val Ala 785 790 795 800

get get geg tit gaa aga aac ggt tet eet ete eea aca aaa eeg caa 2448

Ala Ala Phe Glu Arg Asn Gly Ser Pro Leu Pro Thr Lys Pro Gln 805 810 815

ctt gat atg atc tta gta gag aaa gat tca tgg att tca act gaa gat 2496

Leu Asp Met Ile Leu Val Glu Lys Asp Ser Trp Ile Ser Thr Glu Asp 820 825 830

aat gac tca gag att cgt tta ttg aat tca aga acc aac gga aac gtt 2544

Asn Asp Ser Glu Ile Arg Leu Leu Asn Ser Arg Thr Asn Gly Asn Val 835 840 845

cat	cac	aag	tct	ccg	aaa	cta	gc t	cta	ttc	gca	aca	aac	atc	ac	a a	a t	2592
His	His 850	Lys	Ser	Pro	Lys	Leu 855	Ala	Leu	Phe	Ala	Thr 860	Asn	Ile	Thr	As	n	
tcg	gag	ttc	gac	aga	gct	aaa	tcc	gca	gga	ttt	gca	gat	ace	g gt	a a	t a	2640
Ser 865	Glu	Phe	Asp	Arg	Ala 870	Lys	Ser	Ala	Gly	Phe 875	Ala	Asp	Thr	Val	I 1 88		
atg	aaa	ccg	tta	aga	gca	agc	atg	att	ggg	gcg	gtgt	ctg	g caa	a ca	a g	;t t	2688
Met	Lys	Pro	Leu	Arg 885	Ala	Ser	Met	Ile	Gly 890	Ala	Cys	Leu	Gln	Glr 895		ıl	
ctc	gag	ctg	aga	aaa	aca	aga	. caa	caa	ı cat	cca	ı gaa	ı gga	a te	a to	ca c	cc	2736
Leu	Glu	Leu	Arg 900		Thr	Arg	Gln	Gln 905	His	Pro	Glu	Gly	Ser 910		r Pi	ro	
gca	. act	ctc	aag	g ago	tte	g cti	aca	ı ggg	g aag	g aag	g at	t ct	t gt	g gt	tt g	gat	2784
Ala	Thr	Leu 915		Ser	Leu	Leu	Thr 920		Lys	Lys	Ile	Leu 925		Va	l As	sp	

gat	aat	ata	gtt	aac	agg	aga	gta	gct	gca	gga	gct	ctc	aag	aaa	ttt	2832
Asp	Asn 930	Ile	Val	Asn	Arg	Arg 935	Val	Ala	Ala		Ala 940	Leu	Lys	Lys	Phe	
gga	gca	gaa	gtg	gtt	tgt	gca	gag	agt	ggt	caa	gtt	gct	ttg	ggt	ttg	2880
Gly 945	Ala	Glu	Val	Val	Cys 950	Ala	Glu	Ser	Gly	Gln 955	Val	Ala	Leu	Gly	Leu 960	
ctt	cag	att	cca	cac	ac t	ttc	gat	gct	tgc	ttc	atg	gat	att	caa	atg	2928
Leu	Gln	Ile	Pro	His	Thr	Phe	Asp	Ala	Cys	Phe	Met	Asp	Ile	Gln	Met	
				965					970					975		
cca	cag	atg	gac		t t t	gaa	gca	ac t		cag	ata	aga	atg		gag	2976
				gga		•			cgt			Arg		atg		2976
Pro	Gln	Met	Asp 980	gga Gly	Phe	Glu	Ala	Thr 985	cgt Arg	Gln	Ile	Arg	Me t 990	atg Met		2976 3024
Pro	Gln	Met	Asp 980 aaa	gga Gly gag	Phe	Glu acg Thr	Ala	Thr 985 ctc	cgt Arg	Gln	Ile cat His	Arg	Met 990 ccg	atg Met	Glu	

Ala Met Thr Ala Asp Val Ile His Ala Thr Tyr Glu Glu Cys Leu Lys 1010 1015 1020

agt ggg atg gat ggt tac gtc tcc aaa cct ttt gaa gaa gag aat ctc 3120

Ser Gly Met Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Asn Leu 1025 1030 1035 1040

tat aaa tcc gtt gcc aaa tca ttc aaa cct aat cct atc tca cct tcg 3168

Tyr Lys Ser Val Ala Lys Ser Phe Lys Pro Asn Pro Ile Ser Pro Ser 1045 1050 1055

tcg taa 3174

Ser

<210> 6

<211> 1057

<212> PRT

<213> Arabidopsis thaliana

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Met Asn Trp Ala Leu Asn Asn His Gln Glu Glu Glu Glu Pro Arg

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Asp	Phe	Tyr	Gln	Leu	Gly	Gly	Gly	Gly	Ala	Leu	Asn	Ser	Ser	Glu	Lys
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Pro	Arg	Lys	Ile	Asp	Phe	Trp	Arg	Ser	Gly	Leu	Me t	Gly	Phe	Ala	Lys
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Met	Gln	Gln	Gln	Gln	Gln	Leu	Gln	His	Ser	Val	Ala	Val	Lys	Met	Asn
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Asn	Asn	Asn	Asn	Asn	Asp	Leu	Met	Gly	Asn	Lys	Lys	Gly	Ser	Thr	Phe
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Ile	Gln	Glu	His	Arg	Ala	Leu	Leu	Pro	Lys	Ala	Leu	Ile	Leu	Trp	Ile
			100					105					110		
Ile	Ile	Val	Gly	Phe	Ile	Ser	Ser	Gly	Ile	Tyr	Gln	Trp	Met	Asp	Asp
		115					120					125			
Ala	Asn	Lys	Ile	Arg	Arg	Glu	Glu	Val	Leu	Val	Ser	Met	Cys	Asp	Gln
	130					135					140				
Arg	Ala	Arg	Met	Leu	Gln	Asp	Gln	Phe	Ser	Val	Ser	Val	Asn	His	Val
145					150					155					160
His	Ala	Leu	Ala	Ile	Leu	Val	Ser	Thr	Phe	His	Tyr	His	Lys	Asn	Pro
				165					170					175	
Ser	Ala	Ile	Asp	Gln	Glu	Thr	Phe	Ala	Glu	Tyr	Thr	Ala	Arg	Thr	Ala
			180					185					190		
Phe	Glu	Arg	Pro	Leu	Leu	Ser	Gly	Val	Ala	Tyr	Ala	Glu	Lys	Val	Val
		195					200					205			
Asn	Phe	Glu	Arg	Glu	Met	Phe	Glu	Arg	Gln	His	Asn	Trp	Val	He	Lys

	210					215					220				
Thr	Met	Asp	Arg	Gly	Glu	Pro	Ser	Pro	Val	Arg	Asp	Glu	Tyr	Ala	Pro
225					230					235					240
Val	Ile	Phe	Ser	Gln	Asp	Ser	Val	Ser	Tyr	Leu	Glu	Ser	Leu	Asp	Met
				245					250					255	
Met	Ser	Gly	Glu	Glu	Asp	Arg	Glu	Asn	Ile	Leu	Arg	Ala	Arg	Glu	Thr
			260					265					270		
Gly	Lys	Ala	Val	Leu	Thr	Ser	Pro	Phe	Arg	Leu	Leu	Glu	Thr	His	His
		275					280					285			
Leu	Gly	Val	Val	Leu	Thr	Phe	Pro	Val	Tyr	Lys	Ser	Ser	Leu	Pro	Glu
	290					295					300				
Asn	Pro	Thr	Val	Glu	Glu	Arg	Ile	Ala	Ala	Thr	Ala	Gly	Tyr	Leu	Gly
305					310					315					320
Gly	Ala	Phe	Asp	Val	Glu	Ser	Leu	Val	Glu	Asn	Leu	Leu	Gly	Gln	Leu
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Ala	Gly	Asn	Gln	Ala	Ile	Val	Val	His	Val	Tyr	Asp	Ile	Thr	Asn	Ala
			340					345		•			350		
Ser	Asp	Pro	Leu	Val	Met	Tyr	Gly	Asn	Gln	Asp	Glu	Glu	Ala	Asp	Arg
		355					360					365			
Ser	Leu	Ser	His	Glu	Ser	Lys	Leu	Asp	Phe	Gly	Asp	Pro	Phe	Arg	Lys
	370					375					380				
His	Lys	Met	Ile	Cys	Arg	Tyr	His	Gln	Lys	Ala	Pro	Ile	Pro	Leu	Asn
385					390					395					400
Val	Leu	Thr	Thr	Val	Pro	Leu	Phe	Phe	Ala	Ile	Gly	Phe	Leu	Val	Gly
				405					410					415	
Tyr	Ile	Leu	Tyr	Gly	Ala	Ala	Met	His	Ile	Val	Lys	Val	Glu	Asp	Asp

			420					425					430		
Phe	His	Glu	Met	Gln	Glu	Leu	Lys	Val	Arg	Ala	Glu	Ala	Ala	Asp	Val
		435					440					445			
Ala	Lys	Ser	Gln	Phe	Leu	Ala	Thr	Val	Ser	His	Glu	Ile	Arg	Thr	Pro
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Met	Asn	Gly	Ile	Leu	Gly	Me t	Leu	Ala	Met	Leu	Leu	Asp	Thr	Glu	Leu
465					470					475					480
Ser	Ser	Thr	Gln	Arg	Asp	Tyr	Ala	Gln	Thr	Ala	Gln	Val	Cys	Gly	Lys
				485					490					495	
Ala	Leu	He	Ala	Leu	Ile	Asn	Glu	Val	Leu	Asp	Arg	Ala	Lys	Ile	Glu
			500					505					510		
Ala	Gly	Lys	Leu	Glu	Leu	Glu	Ser	Val	Pro	Phe	Asp	Ile	Arg	Ser	Ile
		515					520					525			
Leu	Asp	Asp	Val	Leu	Ser	Leu	Phe	Ser	Glu	Glu	Ser	Arg	Asn	Lys	Gly
	530					535					540				
Ile	Glu	Leu	Ala	Val	Phe	Val	Ser	Asp	Lys	Val	Pro	Glu	Ile	Val	Lys
545					550					555					560
Gly	Asp	Ser	Gly	Arg	Phe	Arg	Gln	Ile	Ile	Ile	Asn	Leu	Val	Gly	Asn
				565					570					575	
Ser	Val	Lys	Phe	Thr	Glu	Lys	Gly	His	Ile	Phe	Val	Lys	Val	His	Leu
			580					585					590		
Ala	Glu	Gln	Ser	Lys	Asp	Glu	Ser	Glu	Pro	Lys	Asn	Ala	Leu	Asn	Gly
		595					600					605			
Gly	Val	Ser	Glu	Glu	Met	Ile	Val	Val	Ser	Lys	Gln	Ser	Ser	Tyr	Asn
	610					615					620				
Thr	Leu	Ser	Glv	Tvr	Glu	Ala	Ala	Asp	Glv	Arg	Asn	Ser	Trp	Asp	Ser

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Phe	Lys	His	Leu	Val	Ser	Glu	Glu	Gln	Ser	Leu	Ser	Glu	Phe	Asp	Ile
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Ser	Ser	Asn	Val	Arg	Leu	Met	Val	Ser	He	Glu	Asp	Thr	Gly	Ile	Gly
			660					665					670		
Ile	Pro	Leu	Val	Ala	Gln	Gly	Arg	Val	Phe	Met	Pro	Phe	Met	Gln	Ala
		675					680					685			
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	690					695					700				
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Ser	Arg	Pro	His	Ile	Gly	Ser	Thr	Phe	Trp	Phe	Thr	Ala	Val	Leu	Glu
				725					730					735	
Lys	Cys	Asp	Lys	Cys	Ser	Ala	Ile	Asn	His	Me t	Lys	Lys	Pro	Asn	Val
			740					745					750		
Glu	His	Leu	Pro	Ser	Thr	Phe	Lys	Gly	Me t	Lys	Ala	Ile	Val	Val	Asp
		755					760					765			
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	770					775					780				
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785					790					795					800
Ala	Ala	Ala	Phe	Glu	Arg	Asn	Gly	Ser	Pro	Leu	Pro	Thr	Lys	Pro	Gln
				805					810					815	
Leu	Asp	Met	lle	Leu	Val	Glu	Lys	Asp	Ser	Trp	He	Ser	Thr	Glu	Asp
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Asn	Asn	Ser	Gln	He	Arø	Len	Len	Asn	Ser	Arg	Thr	Asn	Glv	Asn	Val

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Met	Lys	Pro	Leu	Arg	Ala	Ser	Met	Ile	Gly	Ala	Cys	Leu	Gln	Gln	Val
				885					890					895	
Leu	Glu	Leu	Arg	Lys	Thr	Arg	Gln	Gln	His	Pro	Glu	Gly	Ser	Ser	Pro
			900					905					910		
Ala	Thr	Leu	Lys	Ser	Leu	Leu	Thr	Gly	Lys	Lys	Ile	Leu	Val	Val	Asp
		915					920					925			
Asp	Asn	Ile	Val	Asn	Arg	Arg	Val	Ala	Ala	Gly	Ala	Leu	Lys	Lys	Phe
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Gly	Ala	Glu	Val	Val	Cys	Ala	Glu	Ser	Gly	Gln	Val	Ala	Leu	Gly	Leu
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Leu	Gln	Ile	Pro	His	Thr	Phe	Asp	Ala	Cys	Phe	Met	Asp	Ile	Gln	Met
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Pro	Gln	Met	Asp	Gly	Phe	Glu	Ala	Thr	Arg	Gln	Ile	Arg	Me t	Met	Glu
			980					985					990		
Lys	Glu	Ala	Lys	Glu	Lys	Thr	Asn	Leu	Glu	Trp	His	Leu	Pro	Ile	Leu
		995				1	000				1	005			
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1045 1050 1055

Ser

<210> 7

<211> 125

<212> PRT

<213> Saccharomyces cerevisiae

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Leu Ala Cys Asp Gly Gln Glu Ala Phe Asp Lys Val Lys Glu Leu Thr

35
40
45

Ser Lys Gly Glu Asn Tyr Asn Met Ile Phe Met Asp Val Gln Met Pro
50 55 60

Lys Val Asp Gly Leu Leu Ser Thr Lys Met Ile Arg Arg Asp Leu Gly
65 70 75 80

Tyr Thr Ser Pro Ile Val Ala Leu Thr Ala Phe Ala Asp Asp Ser Asn 85 90 95

Ile Lys Glu Cys Leu Glu Ser Gly Met Asn Gly Phe Leu Ser Lys Pro 100 105 110

Ile Lys Arg Pro Lys Leu Lys Thr Ile Leu Thr Glu Phe
115 120 125

<210> 8

<211> 118

<212> PRT

<213> Escherichia coli

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Asp Ile Val Leu Ser Asp Val Asn Met Pro Asn Met Asp Gly Tyr Arg

65

Leu Thr Gln Arg Ile Arg Gln Leu Gly Leu Thr Leu Pro Val Ile Gly 70

80 75

Val Thr Ala Asn Ala Leu Ala Glu Glu Lys Gln Arg Cys Leu Glu Ser 90 85

95

Gly Met Asp Ser Cys Leu Ser Lys Pro Val Thr Leu Asp Val Ile Lys

100

105

110

Gln Ser Leu Thr Leu Tyr

115

**<**210**>** 9

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oligonucleotide primer for PCR

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⟨211⟩ 33

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## oligonucleotide primer for PCR

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**⟨400⟩** 18

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32

<210> 19

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⟨211⟩ 31
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